

-1-

SEQUENCE LISTING

<110> ICOS Corporation, et al.

<120> MACROPHAGE DERIVED CHEMOKINE (MDC), MDC ANALOGS, MDC INHIBITOR SUBSTANCES, AND USES THEREOF

<130> 27866/34810PCT

<140>

<141>

<150> 09/067,447

<151> 1998-04-28

<150> 08/939,107

<151> 1997-09-26

<150> 08/660,542

<151> 1996-06-07

<150> 08/558,658

<151> 1995-11-16

<150> 08/479,620

<151> 1995-06-07

<160> 46

<170> PatentIn Ver. 2.0

<210> 1

<211> 2923

<212> DNA

<213> Homo sapiens - human MDC cDNA

<220>

<221> CDS

<222> (20)..(298)

<220>

<221> mat_peptide

<222> (92)..(298)

<400> 1

gagacataca ggacagage atg gct cgc cta cag act gca ctc ctg gtt gtc 52
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-20 -15

ctc gtc ctc ctt gtc gcg ctt caa gca act gag gca ggc ccc tac 100
Leu Val Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr
-10 -5 -1 1

-2-

ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat	tac gtc cgt tac	148
Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp	Tyr Val Arg Tyr	
5	10	15
cgf ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc		196
Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser		
20	25	30
35		
tgc ccg agg cct ggc gtg gtg cta acc ttc agg gat aag gag atc		244
Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile		
40	45	50
tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg		292
Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu		
55	60	65
agc caa tgaagagcct actctgtatga ccgtggcctt ggctcctcca ggaaggctca		348
Ser Gln		
ggagccctac ctccctgcca ttatagctgc tccccggcag aagcctgtgc caactctctg		408
cattccatga tctccatccc tgtggctgtc acccttggtc acctccgtgc tgtcaactgcc		468
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-3-

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<210> 2

<211> 93

<212> PRT

<213> Homo sapiens - human MDC

-4-

<400> 2
Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Ala
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
-5 -1 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 3
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer JHSP6

<400> 3
gacactatag aatagggc 18

<210> 4
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer M13

<400> 4
gtaaaacgac ggccagt 17

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer T3.1

<400> 5
aattaaccct cactaaagg 20

-5-

<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer T7.1

<400> 6
gtaatacgac tcactatagg gc

22

<210> 7
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-1F

<400> 7
tctatctaga ggcccctacg gcgccaacat ggaag

35

<210> 8
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-2R

<400> 8
caccggatcc tcattggctc agcttattga gaa

33

<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-4R

<400> 9
aatggatcca cagcacggag gtgaccaag

29

<210> 10
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-3R

-6-

<400> 10
agtcaagctt agggcactct gggatcgca c

31

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-FX2

<400> 11
tatcggatcc tggttccgcg tggccctac ggcccaaca tggaa

45

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer GEX5

<400> 12
gaaatccagc aagtatata tag ca

22

<210> 13
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-Pel

<400> 13
attgccatgg ccggccctta cggcccaac atggaa

36

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390RcH

<400> 14
gaccaagctt gagacataca ggacagagca

30

<210> 15
<211> 29
<212> DNA

-7-

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390RcX

<400> 15

tggatctaga agttggcaca ggcttctgg

29

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer DC03

<400> 16

cgaaaattaaat acgactcact

20

<210> 17

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
390mycRX

<400> 17

tggatctaga tcaattcaag tcctcctcgc tgatca gtt ctgctcttgg ctcagcttat 60

tgagaat

67

<210> 18

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-3

<220>

<400> 18

Met Lys Ala Ser Ala Ala Leu Leu Cys Leu Leu Thr Ala Ala Ala
-20 -15 -10Phe Ser Pro Gln Gly Leu Ala Gln Pro Val Gly Ile Asn Thr Ser Thr
-5 1 5Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu
10 15 20 25Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala Val
30 35 40

-8-

Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln
 45 50 55

Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr
 60 65 70

Pro Lys Leu
 75

<210> 19

<211> 99

<212> PRT

<213> Homo spapiens - Hu MCP-1

<400> 19

Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Ile Ala Ala Thr
 -20 -15 -10

Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val
 -5 1 5

Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
 10 15 20 25

Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
 30 35 40

Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
 45 50 55

80

Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
 60 65 70

Pro Lys Thr
 75

<210> 20

<211> 76

<212> PRT

<213> Homo sapiens - Hu MCP-2

<220>

<400> 20

Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val Ile
 1 5 10 15

Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile Thr
 20 25 30

Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg Gly
 35 40 45

Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser Met
 50 55 60

-9-

Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
 65 70 75

<210> 21
 <211> 91
 <212> PRT
 <213> Homo sapiens - RANTES

<220>
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 Met Lys Val Ser Ala Ala Ala Leu Ala Val Ile Leu Ile Ala Thr Ala
 -20 -15 -10

Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro
 -5 1 5

Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys
 10 15 20 25

Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe
 30 35 40

Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp
 45 50 55

Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser
 60 65

<210> 22
 <211> 91
 <212> PRT
 <213> Homo sapiens - MIP-1 beta

<220>
 <400> 22
 Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
 -20 -15 -10

Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
 -15 1 5

Ala Cys Cys Phe Ser Tyr Thr Arg Glu Ala Ser Ser Asn Phe Val Val
 10 15 20

Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe
 30 35 40

Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp
 45 50 55

Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
 60 65

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<210> 23
<211> 92
<212> PRT
<213> Homo sapiens - MIP-1 alpha

<220>
<400> 23

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
-20 -15 -10

Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
-5 1 5 10

Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
15 20 25

Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
30 35 40

Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
45 50 55

Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
60 65 70

<210> 24
<211> 96
<212> PRT
<213> Homo sapiens - I-309

<220>
<400> 24

Met Gln Ile Ile Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met
-20 -15 -10

Trp Pro Glu Asp Val Asp Ser Lys Ser Met Gln Val Pro Phe Ser Arg
-5 1 5

Cys Cys Phe Ser Phe Ala Glu Gln Glu Ile Pro Leu Arg Ala Ile Leu
10 15 20 25

Cys Tyr Arg Asn Thr Ser Ser Ile Cys Ser Asn Glu Gly Leu Ile Phe
30 35 40

Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu Asp Thr Val Gly Trp
45 50 55

Val Gln Arg His Arg Lys Met Leu Arg His Cys Pro Ser Lys Arg Lys
60 65 70

-11-

<210> 25
<211> 93
<212> PRT
<213> Artificial Sequence - Human MDC analog

<220>
<223> The amino acid at position 24 is selected from the group consisting of arg, gly, ala, val, leu, ile, pro, ser, thr, phe, tyr, trp, aspartate, glutamate, asn, gln, cys, and met

<220>
<223> The amino acid at position 27 is independently selected from the group consisting of lys, gly, ala, val, leu, ile, pro, ser, thr, phe, tyr, trp, aspartate, glutamate, asn, gln, cys, and met

<220>
<223> The amino acid at position 30 is independently selected from the group consisting of tyr, ser, lys, arg, his, aspartate, glutamate, asn, gln, and cys

<220>
<223> The amino acid at position 50 is independently selected from the group consisting of glu, lys, arg, his, gly, and ala

<220>
<223> The amino acid at position 59 is independently selected from the group consisting of trp, ser, lys, arg, his, aspartate, glutamate, asn, gln, and cys

<220>
<223> The amino acid at position 60 is independently selected from the group consisting of val, ser, lys, arg, his, aspartate, glutamate, asn, gln, and cys

<400> 25
Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Ala
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
-5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Xaa
10 15 20

Val Val Xaa His Phe Xaa Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

-12-

Val Val Leu Leu Thr Phe Arg Asp Lys Xaa Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Xaa Xaa Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-7F

<400> 26
tattggatcc gttctagctc cctgttctcc

30

<210> 27
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-8R

<400> 27
ccaagaattc ctgcagccac tttctggct c

31

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer ARA1

<400> 28
gcgactctct actgtttctc

20

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer ARA2

<400> 29
cacaggaaac agctatgacc

20

-13-

<210> 30
<211> 70
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Human MDC analog
<400> 30

Leu Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp
1 5 10 15

Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp
20 25 30

Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg
35 40 45

Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile
50 55 60

Leu Asn Lys Leu Ser Gln
65 70

<210> 31
<211> 69
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Human MDC analog
<400> 31

Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr
1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr
20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp
35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Tyr Leu Lys Met Ile Leu
50 55 60

Asn Lys Leu Ser Gln
65

<210> 32
<211> 69
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Human MDC analog
<400> 32

-14-

Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr
 1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys Glu Tyr Phe Tyr Thr
 20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp
 35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu
 50 55 60

Asn Lys Leu Ser Gln
 65

<210> 33

<211> 1677

<212> DNA

<213> Homo sapiens - human CCR4 cDNA

<220>

<221> CDS

<222> (183)..(1262)

<400> 33

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agaaaagcaa gctgcttctg gttggggccca gacctgcctt gaggagcctg tagagttaaa 180

aa atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata 227
 Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile
 1 5 10 15tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa 275
 Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys
 20 25 30gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc 323
 Glu Gly Ile Lys Ala Phe Glu Leu Phe Leu Pro Pro Leu Tyr Ser
 35 40 45ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc 371
 Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val
 50 55 60ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc 419
 Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu
 65 70 75aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg 467
 Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp
 80 85 90 95

-15-

ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag 515
 Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys
 100 105 110

 atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt 563
 Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe
 115 120 125

 gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg 611
 Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val
 130 135 140

 ttt tcc ttg agg gca agg acc ttg act tat ggg gtc atc acc agt ttg 659
 Phe Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu
 145 150 155

 gct aca tgg tca gtg gct gtg ttc gcc tcc ctt cct ggc ttt ctg ttc 707
 Ala Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe
 160 165 170 175

 agc act tgt tat act gag cgc aac cat acc tac tgc aaa acc aag tac 755
 Ser Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr
 180 185 190

 tct ctc aac tcc acg acg tgg aag gtt ctc agc tcc ctg gaa atc aac 803
 Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn
 195 200 205

 att ctc gga ttg gtg atc ccc tta ggg atc atg ctg ttt tgc tac tcc 851
 Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser
 210 215 220

 atg atc atc agg acc ttg cag cat tgt aaa aat gag aag aac aag 899
 Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys
 225 230 235

 gcg gtg aag atg atc ttt gco gtg gtg gtc ctc ttc ctt ggg ttc tgg 947
 Ala Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp
 240 245 250 255

 aca cct tac aac ata gtg ctc ttc cta gag acc ctg gtg gag cta gaa 995
 Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu
 260 265 270

 gtc ctt cag gac tgc acc ttt gaa aga tac ttg gac tat gcc atc cag 1043
 Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln
 275 280 285

 gcc aca gaa act ctg gct ttt gtt cac tgc tgc ctt aat ccc atc atc 1091
 Ala Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile
 290 295 300

 tac ttt ttt ctg ggg gag aaa ttt cgc aag tac atc cta cag ctc ttc 1139
 Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe
 305 310 315

aaa acc tgc agg ggc ctt ttt gtg ctc tgc caa tac tgt ggg ctc ctc 1187
 Lys Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu
 320 325 330 335

caa att tac tct gct gac acc ccc agc tca tct tac acg cag tcc acc 1235
 Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr
 340 345 350

atg gat cat gat ctt cat gat gct ctg tagaaaaat gaaatggtga 1282
 Met Asp His Asp Leu His Asp Ala Leu
 355 360

aatgcagagt caatgaactt ttccacatc agagcttact taaaattgg tatttttagg 1342
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 ctcatcctgc aggcagctt ttctctccca ctagacaagt ccagcctggc aagggttcac 1462
 ctgggctgag gcatccttcc tcacaccagg cttgcctgca ggcatgagtc agtctgatga 1522
 gaactctgag cagtgcgtga atgaagttgt aggtaatatt gcaaggcaaa gactattccc 1582
 ttctaacctg aactgatggg tttctccaga gggattgca gagtactggc tcatggagta 1642
 aatcgctacc tttgctgtg gcaaattggc ccccg 1677

<210> 34

<211> 360

<212> PRT

<213> Homo sapiens - human CCR4

<400> 34

Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
 1 5 10 15

Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
 20 25 30

Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
 35 40 45

Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
 50 55 60

Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
 65 70 75 80

Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
 85 90 95

-17-

Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
 100 105 110

Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
 115 120 125

Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
 130 135 140

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
 145 150 155 160

Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
 165 170 175

Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
 180 185 190

Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
 195 200 205

Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
 210 215 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
 225 230 235 240

Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
 245 250 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
 260 265 270

Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
 275 280 285

Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
 290 295 300

Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
 305 310 315 320

Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
 325 330 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
 340 345 350

Asp His Asp Leu His Asp Ala Leu
 355 360

<210> 35
 <211> 1784

-18-

<212> DNA

<213> murine MDC cDNA

<220>

<221> CDS

<222> (1) .. (276)

<220>

<221> mat_peptide

<222> (73) .. (276)

<400> 35

atg tct aat ctg cgt gtc cca ctc ctg gtg gct ctc gtc ctt ctt gct 48
Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Ala
-20 -15 -10

gtg gca att cag acc tct gat gca ggt ccc tat ggt gcc aat gtg gaa 96
Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu
-5 -1 1 5

gac agt atc tgc tgc cag gac tac atc cgt cac cct ctg cca tca cgt 144
Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg
10 15 20

tta gtg aag gag ttc ttc tgg acc tca aaa tcc tgc cgc aag cct ggc 192
Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly
25 30 35 40

gtt gtt ttg ata acc gtc aag aac cga gat atc tgt gcc gat ccc agg 240
Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg
45 50 55

cag gtc tgg gtg aag aag cta ctc cat aaa ctg tcc tagggaggag 286
Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser
60 65

gacctgatga ccatgggtct ggtgggtcc agggaggctc agcaagccct attcttctgc 346

cattccagca agagccttgc caacgacgcc acctttactc acctccatcc cctgggtgt 406

cactctgtca ggctctggtc ctcttacctc cctctatacc ctteccagett atcccccttc 466

aatgtggcag ctgggaaaca cattcaggcc agccttaccc aatgcctact ccccaactgct 526

ttagatgaga ccagcgctt tggtttgatg ccctgatctt atgatgcctt ccccatcccc 586

agccttggcc cccttctctt cttgcatgta gggaaaggccc ataggttca aatatgtgct 646

acctacttcc ctttctgggg ggttctaata cccagcatgt ttttcctgct gcaggcacct 706

atccagtgcc acacacccctcc caagttctta tcagtcctcag tggcatcca ccaagcccc 766

aacttcagac ttcccttggcc tccacctact ctcagtagaa ttctggaggt ttcaggctgg 826

tccaccaggc cccccaggggt taggccaagg tccccaccag agctccctcct gtttcttgg 886

-19-

ctgcagcacg gggcagggag caaggagcag gctcagaatc agatttctta aaggagctgc 946
 agactccatc agtaaaagga atctttctcc catccctgaa tataaggcag tttctgtca 1006
 acacagagac tcaggttgtt agaaatggcc acatagatca actgtgaaac cctaaattta 1066
 ccaagaatca acttccaccc ctcttcaacc acatgctagg gtctttact ttctctgccc 1126
 cacacccggg actccttgcc tgtgttagctg atagtcgaag ttatgctatg gtgtcagtga 1186
 ctgccacagt ttgtttggta ttataagcta tagttatatt tatataaggaa agaggataaa 1246
 tatatgtggg ccaaataagac gaactggaga gttttaggat ctggggcag gaaggccat 1306
 acaaagtgtat acctcagaaa atagatggtt gtggagctg ctgccagtgg cagagttaac 1366
 ttaaagaact taattgaaat tatttttagt tggctgaggg caagacaaga atatagaacc 1426
 cattcttgct tccctggaga caacagtggt cccagggaa ggaataaacc ttcttgctcc 1486
 tctggaggga gcatggcctg rcttagccga gtgactggac tgtgtgagat tggggccatc 1546
 gctttcccty tctgagccctc agctgacagc atatggacc acaaagggt tgatccaaac 1606
 cacagggatt gacagtgcac gcccacagctg tgtccagggc tcgtgttctg ccagaaggag 1666
 cacctggacg accagggcca ccactagtgc tactttgctc actgcccattc catgtcctga 1726
 aggtccctcc ccctcctctc ctacttctgg gaaaataaat gctcgccaaat aatacctg 1784

<210> 36

<211> 92

<212> PRT

<213> murine MDC

<400> 36

Met	Ser	Asn	Leu	Arg	Val	Pro	Leu	Leu	Val	Ala	Leu	Val	Leu	Leu	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

-20

-15

-10

Val	Ala	Ile	Gln	Thr	Ser	Asp	Ala	Gly	Pro	Tyr	Gly	Ala	Asn	Val	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

-5

-1

1

5

Asp	Ser	Ile	Cys	Cys	Gln	Asp	Tyr	Ile	Arg	His	Pro	Leu	Pro	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

10

15

20

Leu	Val	Lys	Glu	Phe	Phe	Trp	Thr	Ser	Lys	Ser	Cys	Arg	Lys	Pro	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

25

30

35

40

Val	Val	Leu	Ile	Thr	Val	Lys	Asn	Arg	Asp	Ile	Cys	Ala	Asp	Pro	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

45

50

55

Gln	Val	Trp	Val	Lys	Lys	Leu	Leu	His	Lys	Leu	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

60

65

SUBSTITUTE SHEET (RULE 26)

-20-

<210> 37
 <211> 958
 <212> DNA
 <213> rat MDC cDNA

<220>
 <221> CDS
 <222> (1)..(243)

<220>
 <221> mat_peptide
 <222> (40)..(243)

<400> 37
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 -10 -5 -1 1

ggt gcc aat gtg gaa gac agt atc tgc tgc cag gac tac atc cgt cac 96
 Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His
 5 10 15

cct ctg cca cca cgt ttc gtg aag gag ttc tac tgg acc tca aag tcc 144
 Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser
 20 25 30 35

tgc cgc aag cct ggc gtc gtt ttg ata acc atc aag aac cga gat atc 192
 Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile
 40 45 50

tgt gct gac ccc ang atg ctc tgg gtg aag aag ata ctc cac aag ttg 240
 Cys Ala Asp Pro Xaa Met Leu Trp Val Lys Lys Ile Leu His Lys Leu
 55 60 65

gcc tagggagaag ggcctgatga ccacgggtct ggtgtctcca caaggctcag 293
 Ala

caaaccctat ctttgcac tccagcaaga gccttgcac caactccacc tttgctcacc 353

tccatccccct gggttgtcac tctgtgaagc ctcgggtccc tgtacttcct gtccgtcccc 413

tccagctcat tctttccaa cgtggcagcc gggaaagcaact tctggcttagc cttacccaat 473

actactcccc actgctttaa atgagaccag ggtcctgtt ttgggtgcctt tggatcctat 533

gatgccttcc cagtctccag ctttggcccc cttctttct tacatgttagg gaacaccaat 593

atcttcaag tatgtgtcac ccaatttctc ttcttcggag gctgctggga cccgaaatat 653

tatccctgc tgcaggcctc tccaagcacc actcacccctc caggcttcc atccgtcccc 713

gtcccaagcc ccatgottca gaacttccct tggccccccc ctacactcca caaattctgg 773

ggaagtctca cnaactgggt cccctcaggc ccccacggga aggaaggtcc cccnccaaca 833

-21-

acntccttcct gttttccccg gtctcccncc nccgggantt gggcncccna atccccaaatt 893
tctgaanang aacngcccat tcntcccnntt aaaatthaacc tttccccccc tccctgangt 953
taggn 958

<210> 38
<211> 81
<212> PRT
<213> rat

<400> 38
Leu Val Leu Leu Ala Val Ala Leu Gln Thr Ser Asp Ala Gly Pro Tyr
-10 -5 -1 1

Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His
5 10 15

Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser
20 25 30 35

Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile
40 45 50

Cys Ala Asp Pro Xaa Met Leu Trp Val Lys Lys Ile Leu His Lys Leu
55 60 65

Ala

<210> 39
<211> 506
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: S. cerevisiae alpha factor pre-
pro/human MDC cDNA chimeric construct
<221> CDS
<222> (15)..(476)

<220>
<221> mat_peptide
<222> (270)..(476)
<400> 39

atctcgagct cacg atg aga ttt cct tca att ttt act gca gtt tta ttc 50
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe
-85 -80 -75

gca gca tcc tcc gca tta gct gct cca gtc aac act aca aca gaa gat 98
Ala Ala Ser Ser Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp
-70 -65 -60

-22-

gaa acg gca caa att ccg gct gaa gct gtc atc ggt tac tta gat tta 146
 Glu Thr Ala Gln Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu
 -55 -50 -45

gaa ggg gat ttc gat gtt gct gtt ttg cca ttt tcc aac agc aca aat 194
 Glu Gly Asp Phe Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn
 -40 -35 -30

aac ggg tta ttg ttt ata aat act act att gcc agc att gct gct aaa 242
 Asn Gly Leu Leu Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys
 -25 -20 -15 -10

gaa gaa ggg gta cct ttg gat aaa aga ggc ccc tac ggc ggc aac atg 290
 Glu Glu Gly Val Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met
 -5 -1 1 5

gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac cgt ctg ccc ctg 338
 Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu
 10 15 20

cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc tgc ccc agg cct 386
 Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro
 25 30 35

ggc gtg gtg ttg cta acc ttc agg gat aag gag atc tgt gcc gat ccc 434
 Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro
 40 45 50 55

aga gtg ccc tgg gtg aag atg att ctc aat aag ctg agc caa 476
 Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
 60 65

tgaaggcctt ctagagcggc cgcatcgata 506

<210> 40
 <211> 154
 <212> PRT
 <213> cDNA
 <400> 40
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 -85 -80 -75 -70

Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln
 -65 -60 -55

Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly Asp Phe
 -50 -45 -40

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 -35 -30 -25

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 -20 -15 -10

-23-

Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val
-5 -1 1 5 10

Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys
15 20 25

His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu
30 35 - 40

Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Val Pro Trp
45 50 55

Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 41

<211> 93

<212> PRT

<213> Artificial Human MDC analog

<220>

<223> The amino acid at position 2 is not proline

<220>

<400> 41

Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Ala
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Xaa Tyr Gly Ala Asn Met Glu
-5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 42

<211> 538

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(334)

<220>

-24-

<221> mat_peptide
 <222> (122)...(334)

<400> 42

ccctgagcag agggacctgc acacagagac tccctcctgg gctcctggca cc atg gcc 58
 Met Ala

cca ctg aag atg ctg gcc gtc acc ctc ctc ctg ggg gct tct ctg 106
 Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Gly Ala Ser Leu
 -20 -15 -10

cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc 154
 Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys
 -5 -1 1 5 10

ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg 202
 Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp
 15 20 25

tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act 250
 Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr
 30 35 40

gtg cag ggc agg gcc atc tgt tcg gac ccc aac aac aag aga gtg aag 298
 Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys
 45 50 55

aat gca gtt aaa tac ctg caa agc ctt gag agg tct tgaaggctcc 344
 Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
 60 65 70

tcaccccaaga ctcctgactg tctccggga ctacctggga cctccaccgt tggtgttcac 404

cgcggccacc ctgagcgcct gggtccacgg gaggccttcc agggacgaag aagagccaca 464

gtgagggaga tccccatcccc ttgtctgaac tggagccatg ggcacaaaagg gcccagatta 524

aagtctttat cctc 538

<210> 43

<211> 94

<212> PRT

<213> Homo sapiens

<400> 43

Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Gly Ala
 -20 -15 -10

Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu
 -5 -1 1 5

Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys
 10 15 20 25

-25-

Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe
 30 35 40

Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg
 45 50 55

Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
 60 65 70

<210> 44

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

atgggaccat atggagcaaa tatggaagat agt

33

<210> 45

<211> 335

<212> DNA

<213> Macaque MDC

<220>

<221> CDS

<222> (19)..(297)

<400> 45

agacatacag gacagagc atg gct cgc cta cag act gtg ttc ctg ggt gtc 51
 Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val
 -20 -15

ctc atc ctc ctt got gtg gcg ctt caa gca act gag gca ggc ccc tat 99
 Leu Ile Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr
 -10 -5 -1 1

ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 147
 Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
 5 10 15

cgt atg ccc ctg cgt gtg gtg aaa cac ttc tac tgg acc tca gac tcc 195
 Arg Met Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
 20 25 30 35

tgc ccg agg cct ggc gtg gtg cta acc tcc agg gat aag gag atc 243
 Cys Pro Arg Pro Gly Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile
 40 45 50

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 291
 Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
 55 60 65

-26-

agc caa tgaagagcct actatgatga ccgtggccta agcaagcc
Ser Gln

335

<210> 46

<211> 93

<212> PRT

<213> Macaque MDC

<400> 46

Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val Leu Ile Leu Leu Ala
-24 -20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
-5 -1 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Met Pro Leu Arg
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65